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Patent Application US/08/029,330

SEQUENCE LISTING 1 3 (1) GENERAL INFORMATION: (i) APPLICANT: Burkly, Linda C. 6 (ii) TITLE OF INVENTION: Treatment for Insulin Dependent Diabetes 8 (iii) NUMBER OF SEQUENCES: 8 9 10 (iv) CORRESPONDENCE ADDRESS: 11 12 (A) ADDRESSEE: Allegretti & Witcoff, Ltd. 13 (B) STREET: 10 South Wacker Drive, Suite 3000 (C) CITY: Chicago 14 15 (D) STATE: IL 16 (E) COUNTRY: US (F) ZIP: 60606 17 18 19 (v) COMPUTER READABLE FORM: 20 (A) MEDIUM TYPE: Floppy disk 21 (B) COMPUTER: IBM PC compatible 22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 23 24 (vi) CURRENT APPLICATION DATA: 25 26 (A) APPLICATION NUMBER: 27 (B) FILING DATE: 9 February 1993 28 (C) CLASSIFICATION: 29 30 (viii) ATTORNEY/AGENT INFORMATION: 31 (A) NAME: McNicholas, Janet M. 32 (B) REGISTRATION NUMBER: 32,918 33 (C) REFERENCE/DOCKET NUMBER: 92,749; D015 US 34 35 (ix) TELECOMMUNICATION INFORMATION: 36 (A) TELEPHONE: 312-715-1000 37 (B) TELEFAX: 312-715-1234 38 39 (2) INFORMATION FOR SEQ ID NO:1: 40 (i) SEQUENCE CHARACTERISTICS: 41 42 (A) LENGTH: 360 base pairs (B) TYPE: nucleic acid 43 (C) STRANDEDNESS: single 44 45 (D) TOPOLOGY: linear 46 47 (ii) MOLECULE TYPE: cDNA 48 (ix) FEATURE: (A) NAME/KEY: misc feature 49 50 (B) LOCATION: 1 51 (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy 52 chain variable region; amino acid 1 is Glu (E) but Gln (Q)

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60		, ,	,														
61	GTC	AAA	CTG	CAG	CAG	TCT	GGG	GCA	GAG	CTT	GTG	AAG	CCA	GGG	GCC	TCA	48
62	Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
63	2	_			6		_			11		_		_	16		
64																	
65	GTC	AAG	TTG	TCC	TGC	ACA	GCT	TCT	GGC	TTC	AAC	ATT	AAA	GAC	ACC	TAT	96
66	Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	
67				21					26					31			
68																	
69		CAC					_				_						144
70	Met	His	_	Val	Lys	Gln	Arg		Glu	Gln	Gly	Leu		Trp	Ile	Gly	
71			36					41					46				
72	100	.	63.8	aam	000	. am	999	~~ m	3 CIM		m > m	~ 3 ~	000		mm/1	a a	102
73		ATT															192
74 75	Arg	Ile 51	Авр	Pro	Ald	Ser	56	Asp	1111	гуя	TAL	61	PLO	пув	PIIE	GIII	
76		JI					50					01					
77	GTC	AAG	GCC	ACT	АТТ	ACA	GCG	GAC	ACG	TCC	TCC	AAC	ACA	GCC	TGG	CTG	240
78		Lys															
79	66					71		. •			76				-	81	
80																	
81																	
82	CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	ACT	GCC	GTC	TAC	TAC	TGT	GCA	288
83	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
84					86					91					96		
85																 _	
86		GGA															336
87	Asp	Gly	Met	_	vaı	ser	Tnr	GIY		АТА	Leu	Asp	Pne		GIA	GIN	
88 89				101					106					111			
90	CCC	ACC	ACG	GTC	אַככ	GTC	דרר	тсъ									360
91		Thr		_		_											300
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105 106 107	Val 2		Leu	Gln	Gln 6	Ser	Gly	Ala	Glu	Leu 11	Val	Lys	Pro	Gly	Ala 16	Ser	
108 109 110	Val	Lys	Leu	Ser 21	Cys	Thr	Ala	Ser	Gly 26	Phe	Asn	Ile	Lys	Asp 31	Thr	Tyr	
111 112 113	Met	His	Trp 36	Val	Lys	Gln	Arg	Pro 41	Glu	Gln	Gly	Leu	Glu 46	Trp	Ile	Gly	
114 115 116	Arg	Ile 51		Pro	Ala	Ser	Gly 56	Asp	Thr	Lys	Tyr	Asp 61	Pro	Lys	Phe	Gln	
117 118 119	Val 66	Lys	Ala	Thr	Ile	Thr 71	Ala	Asp	Thr	Ser	Ser 76	Asn	Thr	Ala	Trp	Leu 81	
120 121 122	Gln	Leu	Ser	Ser	Leu 86	Thr	Ser	Glu	Asp	Thr 91	Ala	Val	Tyr	Tyr	Сув 96	Ala	
123 124 125	Asp	Gly	Met	Trp 101	Val	Ser	Thr	Gly	Tyr 106	Ala	Leu	Asp	Phe	Trp 111	Gly	Gln	
126 127 128	Gly	Thr	Thr 116	Val	Thr	Val	Ser	Ser 121									
129 130 131	(2)				FOR CE CI	_											
132 133		•	(<i>I</i>	A) LI 3) TI	ENGTI YPE:	i: 31	l8 ba Leic	ase p	pairs 1	5							
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145 146 147		(ix)		1) N2	E: AME/F DCATI			_fea	ture	•							
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151 152 153	аст				CE DE							ுரார	CTT	тса	CCA	CCA	48
154 155 156					Thr 5												

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157	GAC	AGG	GTT	ACC	ATA	ACC	TGC	AAG	GCC	AGT	CAG	AGT	GTG	ACT	AAT	GAT	96
158	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Thr	Asn	Asp	
159				20					25					30			
160																	
161	GTA	GCT	TGG	TAC	CAA	CAG	AAG	CCA	GGG	CAG	TCT	CCT	AAA	CTG	CTG	ATA	144
162	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	
163			35					40					45				
164																	
165	TAT	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGA	GTC	CCT	GAT	CGC	TTC	ACT	GGC	192
166	Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	
167		50					55					60					
168																	
169	AGT	GGA	TAT	GGG	ACG	GAT	TTC	ACT	TTC	ACC	ATC	AGC	ACT	GTG	CAG	GCT	240
170	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Val	Gln	Ala	
171	65					70					75					80	
172																	
173	GAA	GAC	CTG	GCA	GTT	TAT	TTC	TGT	CAG	CAG	GAT	TAT	AGC	TCT	CCG	TAC	288
174	Glu	Asp	Leu	Ala	Val	Tyr	Phe	Сув	Gln	Gln	Asp	Tyr	Ser	Ser	Pro	Tyr	
175					85					90					95		
176																	
177	ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAG	ATC							318
178	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile							
179				100					105								
180																	
181	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:4	:								
182																	
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183			(i) :	SEQUI	ENCE	CHAI	RACTI	RIST	rics:	:							
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183			(i) :	(A)) LE1		: 106	ami	ino a		3						
183 184			(i) :	(A)	LEI TYI	GTH:	: 106 amino	ami	ino a id		3						
183 184 185			(i) :	(A)	LEI TYI	NGTH:	: 106 amino	ami	ino a id		3						
183 184 185 186				(A)	LEI TYI	NGTH: PE: 6 POLOC	: 106 amino GY:]	ami aci	ino a id ar		3						
183 184 185 186 187				(A) (B) (D)	LEI TYI	NGTH: PE: 6 POLOC	: 106 amino GY:]	ami aci	ino a id ar		3						
183 184 185 186 187 188		(:	Li) 1	(A) (B) (D)	LEI TYI TOI	NGTH: PE: 6 POLOC	: 106 amino 3Y: 3	ami o aci linea	ino a id ar in	acida		ł:					
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183 184 185 186 187 188 189 190	Ser 1	(:	ii) 1 ki) :	(A) (B) (D) MOLE(LEI TYI TOI	NGTH: PE: 6 POLOG TYPE DESG	: 106 amino GY: 3 GY: 3	o aci	ino a id ar in	acida	NO: 4		Val	Ser	Ala 15	Gly	
183 184 185 186 187 188 189 190 191	Ser 1	(:	ii) 1 ki) :	(A) (B) (D) MOLE(LEI TYI TOI CULE ENCE	NGTH: PE: 6 POLOG TYPE DESG	: 106 amino GY: 3 GY: 3	o aci	ino a id ar in	l ID	NO: 4		Val	Ser		Gly	
183 184 185 186 187 188 189 190 191 192 193	1	(: Ile	ii) l ki) l	(A) (B) (D) MOLE(LEI TYI TOI CULE ENCE Thr 5	NGTH: PE: 6 POLOG TYPE DESG	: 106 amino SY: 3 S: pi CRIPT	o aci	ino a id ar in Lys	Q ID Phe 10	NO:4	Leu	_		15		
183 184 185 186 187 188 189 190 191 192 193 194	1	(: Ile	ii) l ki) k Val	(A) (B) (D) MOLEC	LEI TYI TOI CULE ENCE Thr 5	NGTH: PE: 6 POLOG TYPE DESG	: 106 amino SY: 3 S: pi CRIPT	o aci	ino a id ar in Lys	Q ID Phe 10	NO:4	Leu	_		15		
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183 184 185 186 187 188 189 190 191 192 193 194 195 196	1 Asp	(: Ile Arg	ii) l ki) k Val	(A) (B) (D) MOLE SEQUI	LEI TYI TOI TOI TULE Thr 5	NGTH: PE: 6 POLOG TYPE DESG Gln	: 106 amino EY: 3 CRIPT Thr	o ami o aci linea cotei TION:	ino a id ar in ESE(Lys Ala 25	Phe 10	NO:4	Leu	Val	Thr 30	15 Asn	Asp	
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197	1 Asp	(: Ile Arg	ii) l ki) k Val	(A) (B) (D) MOLE SEQUI	LEI TYI TOI TOI TULE Thr 5	NGTH: PE: 6 POLOG TYPE DESG Gln	: 106 amino EY: 3 CRIPT Thr	o ami o aci linea cotei TION:	ino a id ar in ESE(Lys Ala 25	Phe 10	NO:4	Leu	Val	Thr 30	15 Asn	Asp	
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197	1 Asp	(: Ile Arg	ii) l ki) k Val Val	(A) (B) (D) MOLE SEQUI	LEI TYI TOI TOI TULE Thr 5	NGTH: PE: 6 POLOG TYPE DESG Gln	: 106 amino EY: 3 CRIPT Thr	o ami	ino a id ar in ESE(Lys Ala 25	Phe 10	NO:4	Leu	Val Lys	Thr 30	15 Asn	Asp	
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199	1 Asp Val	(i Ile Arg	ti) l ci) l Val Trp 35	(A) (B) (D) MOLE SEQUI	LEI TYI TOI TOI TULE Thr 5 Ile	NGTH: PE: 6 POLOG TYPE DESG Gln Gln	: 106 amino EY: 3 CRIPT Thr Cys	o acidines cote TION: Pro Lys Pro 40	ino a id ar in ESE(Lys Ala 25 Gly	Phe 10 Ser	NO:4 Leu Gln	Leu Ser Pro	Val Lys 45	Thr 30 Leu	15 Asn Leu	Asp Ile	
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200	1 Asp Val	(i Ile Arg	ti) l ci) l Val Trp 35	(A) (B) (D) MOLE SEQUI	LEI TYI TOI TOI TULE Thr 5 Ile	NGTH: PE: 6 POLOG TYPE DESG Gln Gln	: 106 amino EY: 3 CRIPT Thr Cys	o acidines cote TION: Pro Lys Pro 40	ino a id ar in ESE(Lys Ala 25 Gly	Phe 10 Ser	NO:4 Leu Gln	Leu Ser Pro	Val Lys 45	Thr 30 Leu	15 Asn Leu	Asp Ile	
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201	1 Asp Val	(in the second s	ti) l ci) l Val Trp 35	(A) (B) (D) MOLE SEQUI	LEI TYI TOI TOI TULE Thr 5 Ile	NGTH: PE: 6 POLOG TYPE DESG Gln Gln	: 106 amino EY: 3 CRIPT Thr Cys Lys	o acidines cote TION: Pro Lys Pro 40	ino a id ar in ESE(Lys Ala 25 Gly	Phe 10 Ser	NO:4 Leu Gln	Leu Ser Pro	Val Lys 45	Thr 30 Leu	15 Asn Leu	Asp Ile	
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202	1 Asp Val Tyr	(in the second s	ti) l ci) l Val Val Ala	(A) (B) (D) MOLE SEQUI	LEI TYI TOI CULE ENCE Thr 5	NGTH: PE: 6 POLOG TYPE DESG Gln Thr Gln Arg	Thr Cys Tyr 55	o acidines cotes TION: Pro Lys Pro 40	ino a id ir in Lys Ala 25 Gly	Phe 10 Ser Gln	NO:4 Leu Gln Ser	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe	15 Asn Leu Thr	Asp Ile Gly	
183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203	1 Asp Val Tyr	(in the second s	ti) l ci) l Val Val Ala	(A) (B) (D) MOLE SEQUI	LEI TYI TOI CULE ENCE Thr 5	NGTH: PE: 6 POLOG TYPE DESG Gln Thr Gln Arg	Thr Cys Tyr 55	o acidines cotes TION: Pro Lys Pro 40	ino a id ir in Lys Ala 25 Gly	Phe 10 Ser Gln	NO:4 Leu Gln Ser	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe	15 Asn Leu Thr	Asp Ile Gly	
183 184 185 186 187 188 189 190 191 193 194 195 196 197 198 199 200 201 202 203 204	1 Asp Val Tyr	(in the second s	ti) l ci) l Val Val Ala	(A) (B) (D) MOLE SEQUI	LEI TYI TOI CULE ENCE Thr 5	NGTH: PE: 6 POLOG TYPE DESG Gln Arg	Thr Cys Tyr 55	o acidines cotes TION: Pro Lys Pro 40	ino a id ir in Lys Ala 25 Gly	Phe 10 Ser Gln	NO:4 Leu Gln Ser Pro	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe	15 Asn Leu Thr	Asp Ile Gly Ala	
183 184 185 186 187 188 189 190 191 193 194 195 196 197 198 199 200 201 202 203 204 205	Asp Val Tyr Ser 65	(in the second s	ti) i val Val Trp 35 Ala	(A) (B) (D) MOLE SEQUI	LEI TYI TOI TOI TULE ENCE Thr 5 Ile Gln Asn Thr	NGTH: PE: 6 POLOG TYPE DESG Gln Arg Asp 70	Thr Cys Tyr 55 Phe	o acidines cotes TION: Pro 40 Thr	ino aid ar in Eq. Lys Gly Phe	Phe 10 Ser Wal	NO:4 Leu Gln Pro Ile 75	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe Val	15 Asn Leu Thr	Asp Ile Gly Ala 80	
183 184 185 186 187 188 189 190 191 193 194 195 196 197 198 199 200 201 202 203 204 205 206	Asp Val Tyr Ser 65	(in the second s	ti) i val Val Trp 35 Ala	(A) (B) (D) MOLE SEQUI Met Thr 20 Tyr Ser Gly	LEI TYI TOI TOI TULE ENCE Thr 5 Ile Gln Asn Thr	NGTH: PE: 6 POLOG TYPE DESG Gln Arg Asp 70	Thr Cys Tyr 55 Phe	o acidines cotes TION: Pro 40 Thr	ino aid ar in Eq. Lys Gly Phe	Phe 10 Ser Wal	NO:4 Leu Gln Pro Ile 75	Leu Ser Pro Asp 60	Val Lys 45 Arg	Thr 30 Leu Phe Val	15 Asn Leu Thr	Asp Ile Gly Ala 80	

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209																	
210	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile							
211			-	100	•		•		105								
212																	
213	(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	10:5	:								
214																	
215		(i)) SE	DUEN	CE CI	HARA	CTER:	ISTI	CS:								
216			(2	A) LI	ENGTI	H: 42	29 ba	ase j	pair	S							
217			(1	B) T	YPE:	nuc:	leic	aci	d								
218			((C) S:	rani	DEDNI	SSS:	sin	gle								
219			(1) T(DPOL	OGY:	line	ear									
220																	
221		(ii)	MOI	LECUI	LE T	YPE:	cDN2	A									
222																	
223		(ix)		ATURI	_												
224				A) NZ				_	tide								
225			(1	3) L(CAT:	ION:	1	57					•				
226		()			_												
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230			(1	3) L(JCAI.	LON:	50.	.443									
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236		(ix)	(1 (1	A) N2 B) L(AME/I	con:	1	_			"pB	AG19!	5 in:	sert	: AS	heavy	r
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236 237 238 239			(1 (1	A) N2 B) L(AME/I OCATI THER cha	INFO	1 ORMA: varia	- TION able	: /no	ote= ion"	_	AG19!	5 in	sert	: AS	heavy	,
236 237 238 239 240			(1 (1	A) N2 B) L(D) O	AME/I OCATI THER cha	INFO	1 ORMA: varia	- TION able	: /no	ote= ion"	_	AG19!	5 in	sert	: AS	heavy	7
236 237 238 239 240 241	ATG	(x i)	() (1 () SE(A) N2 B) L(D) O	AME/I DCATI THER Cha	INFO	1 ORMA: Varia IPTI(TION able ON:	: /nd reg: SEQ :	ote= ion" ID N	- D:5:					-	48
236 237 238 239 240 241 242		(xi)	() () () SE(A) NI B) L(D) OT	AME/I DCATI THER Cha	INFO ain v SSCRI	1 ORMA: Varia (PTI)	TTC	: /nd reg: SEQ :	ote= ion" ID NO	CTG	GCT	GTA	GCA	CCA	GGT	
236 237 238 239 240 241 242 243 244 245		(xi)	() () () SE(A) NAB) LODO OTA	AME/I DCATI THER Cha	INFO ain v SSCRI	1 ORMA: Varia (PTI)	TTC	: /nd reg: SEQ :	ote= ion" ID NO	CTG	GCT	GTA	GCA	CCA	GGT	
236 237 238 239 240 241 242 243 244 245 246	Met -19	(xi) GAC Asp	() () () SE(TGG Trp	A) NAB) LODO OTA	TGG TTP -15	INFO ain v SSCR: AGG Arg	1 ORMA: Varia OPTIO GTC Val	TION TTC Phe	reg: SEQ : TGC Cys	ote= ion" ID No TTG Leu -10	CTG Leu	GCT Ala	GTA Val	GCA Ala	CCA Pro -5	GGT Gly	48
236 237 238 239 240 241 242 243 244 245 246 247	Met -19 GCC	(xi) GAC Asp	TGG Trp	A) NA B) LO CO	TGG Trp -15	INFO	1 ORMA: Varia CPTIC GTC Val	TION TTC Phe CAG	: /ndreg: SEQ : TGC Cys	ote= ion" ID No TTG Leu -10	CTG Leu GGT	GCT Ala	GTA Val GGT	GCA Ala	CCA Pro -5	GGT Gly AGA	
236 237 238 239 240 241 242 243 244 245 246 247 248	Met -19 GCC	(xi) GAC Asp	TGG Trp	A) NAB) LODO OTA	TGG Trp -15	INFO	1 ORMA: Varia CPTIC GTC Val	TION TTC Phe CAG	: /ndreg: SEQ : TGC Cys	ote= ion" ID No TTG Leu -10	CTG Leu GGT	GCT Ala	GTA Val GGT Gly	GCA Ala	CCA Pro -5	GGT Gly AGA	48
236 237 238 239 240 241 242 243 244 245 246 247 248 249	Met -19 GCC	(xi) GAC Asp	TGG Trp	A) NA B) LO CO	TGG Trp -15	INFO	1 ORMA: Varia CPTIC GTC Val	TION TTC Phe CAG	: /ndreg: SEQ : TGC Cys	ote= ion" ID No TTG Leu -10	CTG Leu GGT	GCT Ala	GTA Val GGT	GCA Ala	CCA Pro -5	GGT Gly AGA	48
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250	Met -19 GCC	(xi) GAC Asp	TGG Trp	A) NA B) LO CO	TGG Trp -15	INFO	1 ORMA: Varia CPTIC GTC Val	TION TTC Phe CAG	: /ndreg: SEQ : TGC Cys	ote= ion" ID No TTG Leu -10	CTG Leu GGT	GCT Ala	GTA Val GGT Gly	GCA Ala	CCA Pro -5	GGT Gly AGA	48
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251	Met -19 GCC Ala	(xi) GAC Asp CAC	TGG Trp	A) NA B) LO CO CUENC ACC Thr CAG Gln 1	TGG Trp -15 GTC Val	INFO	1 ORMA: Varia CTC Val CTG Leu	TION able ON: TTC Phe CAG Gln 5	: /ndreg: SEQ : TGC Cys GAG Glu	ote= ion" ID No TTG Leu -10 AGC Ser	CTG Leu GGT Gly	GCT Ala CCA Pro	GTA Val GGT Gly 10	GCA Ala CTT Leu	CCA Pro -5 GTG Val	GGT Gly AGA Arg	48
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252	Met -19 GCC Ala	(xi) GAC Asp CAC His	TGG Trp TCC Ser	A) NA B) LO C) OT QUENC ACC Thr CAG Gln 1	TGG Trp -15 GTC Val	INFO ain s SCR: AGG Arg CAA Gln	1 DRMA: Varia CPTIC GTC Val CTG Leu	TION able ON: TTC Phe CAG Gln 5	: /ndreg: SEQ: TGC Cys GAG Glu	ote= ion" ID NO TTG Leu -10 AGC Ser	CTG Leu GGT Gly	GCT Ala CCA Pro	GTA Val GGT Gly 10	GCA Ala CTT Leu	CCA Pro -5 GTG Val	GGT Gly AGA Arg	48
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253	Met -19 GCC Ala	(xi) GAC Asp CAC His	TGG Trp TCC Ser	A) NA B) LO CO CUENC ACC Thr CAG Gln 1	TGG Trp -15 GTC Val	INFO ain s SCR: AGG Arg CAA Gln	DRMATORIAL CTG Leu CTG Leu	TION able ON: TTC Phe CAG Gln 5	: /ndreg: SEQ: TGC Cys GAG Glu	ote= ion" ID NO TTG Leu -10 AGC Ser	CTG Leu GGT Gly	GCT Ala CCA Pro	GTA Val GGT Gly 10	GCA Ala CTT Leu	CCA Pro -5 GTG Val	GGT Gly AGA Arg	48
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254	Met -19 GCC Ala	(xi) GAC Asp CAC His	TGG Trp TCC Ser	A) NA B) LO C) OT QUENC ACC Thr CAG Gln 1	TGG Trp -15 GTC Val	INFO ain s SCR: AGG Arg CAA Gln	1 DRMA: Varia CPTIC GTC Val CTG Leu	TION able ON: TTC Phe CAG Gln 5	: /ndreg: SEQ: TGC Cys GAG Glu	ote= ion" ID NO TTG Leu -10 AGC Ser	CTG Leu GGT Gly	GCT Ala CCA Pro	GTA Val GGT Gly 10	GCA Ala CTT Leu	CCA Pro -5 GTG Val	GGT Gly AGA Arg	48
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255	Met -19 GCC Ala CCT Pro	(xi) GAC Asp CAC His	TGG Trp TCC Ser	A) NA B) LO CO CUENC ACC Thr ACC Thr	TGG Trp -15 GTC Val	INFO ain v SCRI AGG Arg CAA Gln	ORMA: Varia OTC Val CTG Leu 20	TION able ON: TTC Phe CAG Gln 5	: /ndreg: SEQ : TGC Cys TGC Cys	ote= ion" ID NO TTG Leu -10 AGC Ser	CTG Leu GGT Gly	GCT Ala CCA Pro	GTA Val GGT Gly 10	GCA Ala CTT Leu TTC Phe	CCA Pro -5 GTG Val	GGT Gly AGA Arg	48 96 144
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256	Met -19 GCC Ala CCT Pro	(xi) GAC Asp CAC His AGC Ser 15	CAG Gln ACC	A) NA B) LO C) OT CUENC ACC Thr ACC Thr TAT	TGG Trp -15 GTC Val CTG Leu	INFO ain v SCR: AGG Arg CAA Gln AGC Ser	1 DRMA: Varia CPTIC GTC Val CTG Leu 20 TGG	TION able ON: TTC Phe CAG Gln 5 ACC Thr	: /ndreg: SEQ: TGC Cys TGC Cys	ote= ion" ID NO TTG Leu -10 AGC Ser ACC Thr	CCA	GCT Ala CCA Pro TCT Ser 25	GTA Val GGT Gly 10 GGC Gly	GCA Ala CTT Leu TTC Phe	CCA Pro -5 GTG Val AAC Asn	GGT Gly AGA Arg ATT Ile	48
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255	Met -19 GCC Ala CCT Pro	(xi) GAC Asp CAC His AGC Ser 15	CAG Gln ACC	A) NA B) LO CO CUENC ACC Thr ACC Thr	TGG Trp -15 GTC Val CTG Leu	INFO ain v SCRI AGG Arg CAA Gln AGC Ser CAC	1 DRMA: Varia CPTIC GTC Val CTG Leu 20 TGG	TION able ON: TTC Phe CAG Gln 5 ACC Thr	: /ndreg: SEQ: TGC Cys TGC Cys	ote= ion" ID NO TTG Leu -10 AGC Ser ACC Thr	CCA	GCT Ala CCA Pro TCT Ser 25	GTA Val GGT Gly 10 GGC Gly	GCA Ala CTT Leu TTC Phe	CCA Pro -5 GTG Val AAC Asn	GGT Gly AGA Arg ATT Ile	48 96 144
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 257	Met -19 GCC Ala CCT Pro	(xi) GAC Asp CAC His AGC Ser 15	CAG Gln ACC	A) NA B) LO C) OT CUENC ACC Thr ACC Thr TAT	TGG Trp -15 GTC Val CTG Leu	INFO ain v SCR: AGG Arg CAA Gln AGC Ser	1 DRMA: Varia CPTIC GTC Val CTG Leu 20 TGG	TION able ON: TTC Phe CAG Gln 5 ACC Thr	: /ndreg: SEQ: TGC Cys TGC Cys	ote= ion" ID NO TTG Leu -10 AGC Ser ACC Thr	CTG Leu GGT Gly GCG Ala CCA Pro	GCT Ala CCA Pro TCT Ser 25	GTA Val GGT Gly 10 GGC Gly	GCA Ala CTT Leu TTC Phe	CCA Pro -5 GTG Val AAC Asn	GGT Gly AGA Arg ATT Ile CTT Leu	48 96 144
236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258	Met -19 GCC Ala CCT Pro AAA Lys 30	(xi) GAC Asp AGC Ser 15 GAC Asp	CAG Gln ACC Thr	A) NA B) LO C) OT CUENC ACC Thr ACC Thr TAT	TGG Trp -15 GTC Val CTG Leu ATG Met	INFO ain s SCR AGG Arg CAA Gln AGC Ser CAC His	1 DRMA: Varia Varia CTC Val CTG Leu 20 TGG Trp	TION able ON: TTC Phe CAG Gln 5 ACC Thr GTG Val	reg: SEQ TGC Cys TGC Cys AGA Arg	ote= ion" ID NO TTG Leu -10 AGC Ser ACC Thr CAG Gln	CCA Pro	GCT Ala CCA Pro TCT Ser 25 CCT Pro	GTA Val GGT Gly 10 GGC Gly	GCA Ala CTT Leu TTC Phe	CCA Pro -5 GTG Val AAC Asn GGT Gly	GGT Gly AGA Arg ATT Ile CTT Leu 45	48 96 144

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261 262	Glu	Trp	Ile	Gly	Arg 50	Ile	Asp	Pro	Ala	Ser 55	Gly	Asp	Thr	Lys	Tyr 60	Asp	
263																	
264 265				CAG Gln			_										288
266	PIO	пур	FIIC	65	Val	ALG	Vai	1111	70	nea	Val	veh	1111	75	per	VOII	
267																	
268	CAG	TTC	AGC	CTG	AGA	CTC	AGC	AGC	GTG	ACA	GCC	GCC	GAC	ACC	GCG	GTC	336
269	Gln	Phe		Leu	Arg	Leu	Ser		Val	Thr	Ala	Ala	_	Thr	Ala	Val	
270 271			80					85					90				
272	TAT	TAT	TGT	GCA	GAC	GGA	ATG	TGG	GTA	TCA	ACG	GGA	TAT	GCT	CTG	GAC	384
273				Ala					_								
274		95			_		100					105					
275																	
276 277				CAA													429
277	110	пр	GIŞ	Gln	GTÅ	1115	THE	Val	IIII	Val	120	per	GTÅ	GIU	ser		
279											110						
280	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:6	:								
281																	
282			(i) S	SEQUI													
283				Ì		NGTH:				acida	3						
284 285				•		PE: 6											
286				(2)		. 020											
287		(:	ii) M	MOLEC	CULE	ТҮРІ	3: pi	rote:	in								
287 288		(:	ii) 1	MOLEC	CULE	TYPI	3: pı	rote:	in								
287 288 289				MOLE(_			Q ID	NO:	5 :					
287 288 289 290	Mot	(2	ki) S	SEQUI	ence	DESC	- CRIP1	rion :	: SE(-			Val	λla	Pro	Glv	
287 288 289 290 291		(2	ki) S		ence	DESC	- CRIP1	rion :	: SE(-			Val	Ala	Pro -5	Gly	
287 288 289 290	Met -19	(2	ki) S	SEQUI	ENCE Trp	DESC	- CRIP1	rion :	: SE(Leu			Val	Ala		Gly	
287 288 289 290 291 292	-19	(s Asp	ki) S	SEQUI	Trp -15	DES(CRIPT	rion: Phe	: SE(Leu -10	Leu	Ala			- 5	_	
287 288 289 290 291 292 293 294 295	-19	(s Asp	ki) S	SEQUI	Trp -15	DES(CRIPT	rion: Phe	: SE(Leu -10	Leu	Ala			- 5	_	
287 288 289 290 291 292 293 294 295 296	-19 Ala	(x Asp His	xi) s Trp Ser	SEQUI Thr Gln	Trp -15 Val	DESC Arg Gln	CRIPT Val Leu	Phe Gln 5	: SE(Cys Glu	Leu -10 Ser	Leu	Ala Pro	Gly 10	Leu	-5 Val	Arg	
287 288 289 290 291 292 293 294 295 296 297	-19 Ala	(x Asp His	xi) s Trp Ser	SEQUI Thr Gln	Trp -15 Val	DESC Arg Gln	CRIPT Val Leu	Phe Gln 5	: SE(Cys Glu	Leu -10 Ser	Leu	Ala Pro	Gly 10	Leu	-5 Val	Arg	
287 288 289 290 291 292 293 294 295 296 297 298	-19 Ala	(x Asp His	xi) s Trp Ser	SEQUI Thr Gln	Trp -15 Val	DESC Arg Gln	CRIPT Val Leu	Phe Gln 5	: SE(Cys Glu	Leu -10 Ser	Leu	Ala Pro	Gly 10	Leu	-5 Val	Arg	
287 288 289 290 291 292 293 294 295 296 297	-19 Ala Pro	Asp His	xi) s Trp Ser	SEQUI Thr Gln	Trp -15 Val	DESC Arg Gln Ser	CRIPT Val Leu 20	Phe Gln 5	Cys Cys	Leu -10 Ser	Leu Gly Ala	Ala Pro Ser 25	Gly 10 Gly	Leu	-5 Val Asn	Arg	
287 288 289 290 291 292 293 294 295 296 297 298 299	-19 Ala Pro	Asp His	xi) s Trp Ser	SEQUI Thr Gln 1	Trp -15 Val	DESC Arg Gln Ser	CRIPT Val Leu 20	Phe Gln 5	Cys Cys	Leu -10 Ser	Leu Gly Ala	Ala Pro Ser 25	Gly 10 Gly	Leu	-5 Val Asn	Arg	
287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302	-19 Ala Pro	Asp His	xi) s Trp Ser	SEQUI Thr Gln 1	Trp -15 Val	DESC Arg Gln Ser	CRIPT Val Leu 20	Phe Gln 5	Cys Cys	Leu -10 Ser	Leu Gly Ala Pro	Ala Pro Ser 25	Gly 10 Gly	Leu	-5 Val Asn	Arg Ile Leu	
287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303	-19 Ala Pro Lys 30	Asp His Ser 15 Asp	ri) some ser	Thr Gln 1 Thr	Trp -15 Val Leu Met	DESC Arg Gln Ser His	Val Leu 20	Phe Gln 5 Thr	Cys Glu Cys	Leu -10 Ser Thr	Leu Gly Ala Pro 40	Ala Pro Ser 25	Gly 10 Gly	Leu Phe Arg	-5 Val Asn Gly	Arg Ile Leu 45	
287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304	-19 Ala Pro Lys 30	Asp His Ser 15 Asp	ri) some ser	SEQUI Thr Gln 1	Trp -15 Val Leu Met	DESC Arg Gln Ser His	Val Leu 20	Phe Gln 5 Thr	Cys Glu Cys	Leu -10 Ser Thr Gln	Leu Gly Ala Pro 40	Ala Pro Ser 25	Gly 10 Gly	Leu Phe Arg	-5 Val Asn Gly	Arg Ile Leu 45	
287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303	-19 Ala Pro Lys 30	Asp His Ser 15 Asp	ri) some ser	Thr Gln 1 Thr	Trp -15 Val Leu Met	DESC Arg Gln Ser His	Val Leu 20	Phe Gln 5 Thr	Cys Glu Cys	Leu -10 Ser Thr	Leu Gly Ala Pro 40	Ala Pro Ser 25	Gly 10 Gly	Leu Phe Arg	-5 Val Asn Gly	Arg Ile Leu 45	
287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305	-19 Ala Pro Lys 30 Glu	Asp His Ser 15 Asp	Trp Ser Gln Thr	Thr Gln 1 Thr	Trp -15 Val Leu Met	DESC Arg Gln Ser His 35	CRIPT Val Leu 20 Trp	Phe Gln 5 Thr Val	Cys Glu Cys Arg	Leu -10 Ser Thr Gln	Leu Gly Ala Pro 40	Ala Pro Ser 25 Pro	Gly Gly Gly	Leu Phe Arg	-5 Val Asn Gly Tyr 60	Arg Ile Leu 45	
287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306	-19 Ala Pro Lys 30 Glu	Asp His Ser 15 Asp	Trp Ser Gln Thr	Thr Gln 1 Thr Gly	Trp -15 Val Leu Met	DESC Arg Gln Ser His 35	CRIPT Val Leu 20 Trp	Phe Gln 5 Thr Val	Cys Glu Cys Arg	Leu -10 Ser Thr Gln	Leu Gly Ala Pro 40	Ala Pro Ser 25 Pro	Gly Gly Gly	Leu Phe Arg	-5 Val Asn Gly Tyr 60	Arg Ile Leu 45	
287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 307 308 309	-19 Ala Pro Lys 30 Glu Pro	Asp His Ser 15 Asp Trp	Trp Ser Ile Phe	Thr Gln Thr Gly Gly Gln 65	Trp -15 Val Leu Met Arg 50 Val	DESC Arg Gln Ser His 35	CRIPT Val Leu 20 Trp Asp Val	Phe Gln Thr Thr	Cys Glu Cys Arg Met 70	Leu -10 Ser Thr Gln Ser 55	Leu Gly Ala Pro 40 Gly Val	Ala Pro Ser 25 Pro Asp	Gly Gly Thr	Leu Phe Arg Lys Ser 75	-5 Val Asn Gly Tyr 60 Ser	Arg Ile Leu 45 Asp	
287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310	-19 Ala Pro Lys 30 Glu Pro	Asp His Ser 15 Asp Trp	Trp Ser Ile Phe	Thr Gln Thr Gly Gly	Trp -15 Val Leu Met Arg 50 Val	DESC Arg Gln Ser His 35	CRIPT Val Leu 20 Trp Asp Val	Phe Gln Thr Thr Ser	Cys Glu Cys Arg Met 70	Leu -10 Ser Thr Gln Ser 55	Leu Gly Ala Pro 40 Gly Val	Ala Pro Ser 25 Pro Asp	Gly 10 Gly Thr	Leu Phe Arg Lys Ser 75	-5 Val Asn Gly Tyr 60 Ser	Arg Ile Leu 45 Asp	
287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 307 308 309	-19 Ala Pro Lys 30 Glu Pro	Asp His Ser 15 Asp Trp	Trp Ser Ile Phe	Thr Gln Thr Gly Gly Gln 65	Trp -15 Val Leu Met Arg 50 Val	DESC Arg Gln Ser His 35	CRIPT Val Leu 20 Trp Asp Val	Phe Gln Thr Thr	Cys Glu Cys Arg Met 70	Leu -10 Ser Thr Gln Ser 55	Leu Gly Ala Pro 40 Gly Val	Ala Pro Ser 25 Pro Asp	Gly Gly Thr	Leu Phe Arg Lys Ser 75	-5 Val Asn Gly Tyr 60 Ser	Arg Ile Leu 45 Asp	

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313 314 315 316	Tyr	Tyr 95	Сув	Ala	Asp	Gly	Met 100	Trp	Val	Ser	Thr	Gly 105	Tyr	Ala	Leu	Asp	
317 318 319	Phe 110	Trp	Gly	Gln	Gly	Thr 115	Thr	Val	Thr	Val	Ser 120		Gly	Glu	Ser		
320 321	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:7	:								
322 323		(i)		QUENC A) L1						6							
324			-	B) T				•	-	5							
325			_	C) S:				_	_								
326			(1) T(DPOL	OGY:	line	ear									
327																	
328		(ii)) MOI	LECUI	LE TY	YPE:	CDN	A									
329 330		(iv	। एक	ATURI	₹•												
331		(IA)		A) N	_	KEY:	sia	pep	tide								
332				B) L(-												
333																	
334		(ix)) FE	ATURI	₫:												
335				A) NZ			_		tide								
336			()	B) L(CAT	ION:	58.	.386									
337 338		(i ~)	\ FF:	ATURI	₽•												
339		(14,		A) Ni	_	KEY:	CDS										
340				B) L(•			386									
341			-	-													
342		(ix)) FE	ATURI	3∶												
343				A) NZ	_			c_fe	atur	е							
344			•	3) L(n=0\	/		n 70 '		.		. 1777) (dinenii	•
345 346			(1	יט נכ			okma: chai:		-		_		3 lna	sert	: VK.	2 (SVMDY)
347					110	311C (,11 Q 11	ı va.	L TaD.	re r	= g ±0,						
348		(xi)	SE(QUENC	CE DI	3SCR	[PTI(ON:	SEQ :	ID NO	0:7:						
349																	
350	ATG	GGT	TGG	TCC	TGC	ATC	ATC	CTG	TTC	CTG	GTT	GCT	ACC	GCT	ACC	GGT	48
351		Gly	Trp	Ser	_	Ile	Ile	Leu	Phe		Val	Ala	Thr	Ala		Gly	
352 353	-19				-15					-10					- 5		
353 354																	
355																	
356	GTC	CAC	TCC	AGC	ATC	GTG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	96
357	Val	His	Ser	Ser	Ile	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	
358				1				5					10				
359	3.44	~m~	~~-	~-		~~~				m~-		~~~	. ~-	~- ~		ama	3 4 4
360 361		GTG Val				_/		_				_		4_			144
362	net	15	GTÅ	voh	ar y	VQI	20	T16	****	Cys	пyр	25	DET	GTII	DET	V G.L	
363		_ _					_ •										
364	ACT	AAT	GAT	GTA	GCT	TGG	TAC	CAG	CAG	AAG	CCA	GGT	AAG	GCT	CCA	AAG	192

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365 366 367	Thr 30	Asn	Asp	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45		
368	CTG	CTG	ATC	TAC	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGT	GTG	CCA	GAT	AGA		240
369				Tyr														
370				_	50					55		_			60			
371																		
372	TTC	AGC	GGT	AGC	GGT	TAT	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC		288
373	Phe	Ser	Gly	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser		
374				65					70					75				
375	~=~													43 =				226
376				GAG														336
377 378	теп	GIN	80	Glu	Asp	TTE	АТа	85	туг	туг	Сув	GIN	90	Asp	туг	ser		
379			80					65					90					
380	тст	CCG	TAC	ACG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	CGT	AAG	TG	386
381				Thr														
382		95	•			•	100	•		•		105		•	-	•		
383																		
384	(2)	INF	ORMA!	rion	FOR	SEQ	ID 1	8:01	:									
385																		
386			(i) :	SEQUI	ENCE	CHAI	RACTI	ERIS'	rics	•								
387				•		NGTH:				acida	3							
388						PE: a												
389				(D)) TOI	POLO	3Y: 3	linea	ar									
390																		
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391		(:	ii) 1	MOLE	CULE	TYPI	3: p	rote	in									
391 392							_			\ TD	NO .	o .						
391 392 393				MOLE SEQUI			_			Q ID	NO:8	3:						
391 392 393 394	Met	(3	ki) S	EQUI	ence	DESC	CRIP	rion:	: SE(_			Thr	Δla	Thr	Glv		
391 392 393 394 395		(3	ki) S		ZNCE Cys	DESC	CRIP	rion:	: SE(Leu			Thr	Ala	Thr	Gly		
391 392 393 394 395 396	Met -19	(3	ki) S	EQUI	ence	DESC	CRIP	rion:	: SE(_			Thr	Ala		Gly		
391 392 393 394 395	-19	() Gly	ki) S	EQUI	Cys -15	DESC	CRIP:	rion: Leu	: SE(Leu -10	Val	Ala			- 5			
391 392 393 394 395 396 397	-19	() Gly	ki) S	SEQUI	Cys -15	DESC	CRIP:	rion: Leu	: SE(Leu -10	Val	Ala			- 5			
391 392 393 394 395 396 397 398	-19	() Gly	ki) S	SEQUI Ser Ser	Cys -15	DESC	CRIP:	FION: Leu Thr	: SE(Leu -10	Val	Ala	Ser		- 5			
391 392 393 394 395 396 397 398 399	-19 Val	Gly His	ri) s	SEQUI Ser Ser	Cys -15	DESC Ile Val	Ile Met	Leu Thr	Phe Gln	Leu -10 Ser	Val Pro	Ala	Ser 10	Leu	-5 Ser	Ala		
391 392 393 394 395 396 397 398 399 400	-19 Val	Gly His	ri) s	SEQUI Ser Ser 1	Cys -15	DESC Ile Val	Ile Met	Leu Thr	Phe Gln	Leu -10 Ser	Val Pro	Ala	Ser 10	Leu	-5 Ser	Ala		
391 392 393 394 395 396 397 398 399 400 401	-19 Val	Gly His	ri) s	SEQUI Ser Ser 1	Cys -15	DESC Ile Val	CRIPS Ile Met	Leu Thr	Phe Gln	Leu -10 Ser	Val Pro	Ala Ser	Ser 10	Leu	-5 Ser	Ala		
391 392 393 394 395 396 397 398 399 400 401 402 403 404	-19 Val Ser	Gly His Val	ri) some	SEQUI Ser Ser 1	Cys -15 Ile	DESC Ile Val	Ile Met Thr	Thr 5	Phe Gln	Leu -10 Ser	Val Pro Lys	Ala Ala 25	Ser 10 Ser	Leu	-5 Ser	Ala Val Lys		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405	-19 Val Ser	Gly His Val	ri) some	SEQUI Ser Ser 1 Asp	Cys -15 Ile	DESC Ile Val	Ile Met Thr	Thr 5	Phe Gln	Leu -10 Ser	Val Pro Lys	Ala Ala 25	Ser 10 Ser	Leu	-5 Ser	Ala Val		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 405	-19 Val Ser	Gly His Val	ri) some	SEQUI Ser Ser 1 Asp	Cys -15 Ile	DESC Ile Val Val	Ile Met Thr	Thr 5	Phe Gln	Leu -10 Ser	Val Pro Lys	Ala Ala 25	Ser 10 Ser	Leu	-5 Ser	Ala Val Lys		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly	SEQUI Ser Ser 1 Asp	Cys -15 Ile Arg	DESC Ile Val Val	Ile Met Thr 20	Leu Thr 5 Ile	Phe Gln Gln	Leu -10 Ser Cys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala	-5 Ser Ser	Ala Val Lys 45		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly	SEQUI Ser Ser 1 Asp	Cys -15 Ile Arg Ala	DESC Ile Val Val	Ile Met Thr 20	Leu Thr 5 Ile	Phe Gln Gln	Leu -10 Ser Cys Lys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala	-5 Ser Ser Pro	Ala Val Lys 45		
391 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly	SEQUI Ser Ser 1 Asp	Cys -15 Ile Arg	DESC Ile Val Val	Ile Met Thr 20	Leu Thr 5 Ile	Phe Gln Gln	Leu -10 Ser Cys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala	-5 Ser Ser	Ala Val Lys 45		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly Asp	SEQUI Ser Ser 1 Asp Val	Cys -15 Ile Arg Ala Tyr 50	DESC Ile Val Val Trp 35	Ile Met Thr 20 Tyr	Leu Thr 5 Ile Gln Asn	Phe Gln Gln Arg	Leu -10 Ser Cys Lys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala Pro	-5 Ser Ser Pro	Ala Val Lys 45		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly Asp	SEQUI Ser Ser 1 Asp Val	Cys -15 Ile Arg Ala Tyr 50	DESC Ile Val Val Trp 35	Ile Met Thr 20 Tyr	Leu Thr 5 Ile Gln Asn	Phe Gln Thr Arg	Leu -10 Ser Cys Lys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala Pro	-5 Ser Ser Pro	Ala Val Lys 45		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412	-19 Val Ser Thr 30	Gly His Val 15 Asn	Trp Ser Gly Asp	SEQUI Ser Ser 1 Asp Val	Cys -15 Ile Arg Ala Tyr 50	DESC Ile Val Val Trp 35	Ile Met Thr 20 Tyr	Leu Thr 5 Ile Gln Asn	Phe Gln Gln Arg	Leu -10 Ser Cys Lys	Val Pro Lys Pro 40	Ala Ser Ala 25 Gly	Ser 10 Ser Lys	Leu Gln Ala Pro	-5 Ser Ser Pro	Ala Val Lys 45		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413	-19 Val Ser Thr 30 Leu	Gly His Val 15 Asn Leu Ser	Trp Ser Gly Gly Gly	SEQUI Ser Ser 1 Asp Val Tyr Ser 65	Cys -15 Ile Arg Ala Tyr 50 Gly	DESC Ile Val Val Trp 35	Ile Met Thr 20 Tyr Ser	Thr 5 Ile Gln Asn Thr	Phe Gln Arg Asp 70	Leu -10 Ser Cys Lys Tyr 55 Phe	Val Pro Lys Pro 40 Thr	Ala Ser Ala 25 Gly Phe	Ser 10 Ser Lys Val	Leu Gln Ala Pro Ile 75	-5 Ser Pro Asp 60 Ser	Ala Val Lys 45 Arg		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412	-19 Val Ser Thr 30 Leu	Gly His Val 15 Asn Leu Ser	Trp Ser Gly Gly Gly	SEQUI Ser Ser 1 Asp Val	Cys -15 Ile Arg Ala Tyr 50 Gly	DESC Ile Val Val Trp 35	Ile Met Thr 20 Tyr Ser	Thr 5 Ile Gln Asn Thr	Phe Gln Arg Asp 70	Leu -10 Ser Cys Lys Tyr 55 Phe	Val Pro Lys Pro 40 Thr	Ala Ser Ala 25 Gly Phe	Ser 10 Ser Lys Val	Leu Gln Ala Pro Ile 75	-5 Ser Pro Asp 60 Ser	Ala Val Lys 45 Arg		
391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 407 408 409 410 411 412 413 414	-19 Val Ser Thr 30 Leu	Gly His Val 15 Asn Leu Ser	Trp Ser Gly Pro	SEQUI Ser Ser 1 Asp Val Tyr Ser 65	Cys -15 Ile Arg Ala Tyr 50 Gly	DESC Ile Val Val Trp 35	Ile Met Thr 20 Tyr Ser	Leu Thr 5 Ile Gln Asn Thr	Phe Gln Arg Asp 70	Leu -10 Ser Cys Lys Tyr 55 Phe	Val Pro Lys Pro 40 Thr	Ala Ser Ala 25 Gly Phe	Ser 10 Ser Lys Val Thr	Leu Gln Ala Pro Ile 75	-5 Ser Pro Asp 60 Ser	Ala Val Lys 45 Arg		

Raw Sequence Listing

04/08/93 07:46:22 S5136.raw

417	Ser Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Lys
418	95					100					105				
419															

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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/029,330

TIME: 07:46:22 S5136

DATE: 04/08/93

LINE ERROR

ORIGINAL TEXT

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SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/08/029,330

TIME: 07:46:22 S5136

DATE: 04/08/93

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/08/029,330

TIME: 07:46:22

DATE: 04/08/93

S5136

CORRECTED TEXT

LINE ORIGINAL TEXT